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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/007,747

DATE: 03/20/2002
TIME: 11:52:40

Input Set : N:\Crf3\RULE60\10007747.raw
Output Set: N:\CRF3\03202002\J007747.raw

SEQUENCE LISTING

- 1 (1) GENERAL INFORMATION:
 - 2 (i) APPLICANT: Daggett, Lorrie P.
3 Ellis, Steven B.
4 Liaw, Chen W.
5 Lu, Chin-Chun
 - 6 (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
7 SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
 - 8 (iii) NUMBER OF SEQUENCES: 63
 - 9 (iv) CORRESPONDENCE ADDRESS:
 - 10 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
 - 11 (B) STREET: 4250 Executive Square, 7th Floor
 - 12 (C) CITY: La Jolla
 - 13 (D) STATE: CA
 - 14 (E) COUNTRY: USA
 - 15 (F) ZIP: 92037
 - 16 (v) COMPUTER READABLE FORM:
 - 17 (A) MEDIUM TYPE: Floppy disk
 - 18 (B) COMPUTER: IBM PC compatible
 - 19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - 20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - 21 (vi) CURRENT APPLICATION DATA:
 - 22 (A) APPLICATION NUMBER: US/10/007,747
 - 23 (B) FILING DATE: 07-Dec-2001
 - 24 (vii) PRIOR APPLICATION DATA:
 - 25 (A) APPLICATION NUMBER: US/09/648,797
 - 26 (B) FILING DATE: 28-Aug-2000
 - 27 (A) APPLICATION NUMBER: US/08/940,086A
 - 28 (B) FILING DATE: 29-SEPT-97
 - 29 (A) APPLICATION NUMBER: US 08/231,193
 - 30 (B) FILING DATE: 20-APR-1994
 - 31 (A) APPLICATION NUMBER: US 08/052,449
 - 32 (B) FILING DATE: 20-APR-1993
 - 33 (viii) ATTORNEY/AGENT INFORMATION:
 - 34 (A) NAME: Seidman, Stephanie
 - 35 (B) REGISTRATION NUMBER: 33,779
 - 36 (C) REFERENCE/DOCKET NUMBER: 24735-9383C
 - 37 (ix) TELECOMMUNICATION INFORMATION:
 - 38 (A) TELEPHONE: (619) 450-8400
 - 39 (B) TELEFAX: (619) 450-8499
 - 40 (2) INFORMATION FOR SEQ ID NO: 1:
 - 41 (i) SEQUENCE CHARACTERISTICS:
 - 42 (A) LENGTH: 4298 base pairs

ENTERED

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43 (B) TYPE: nucleic acid
44 (C) STRANDEDNESS: both
45 (D) TOPOLOGY: both
46 (ii) MOLECULE TYPE: cDNA
47 (ix) FEATURE:
48 (A) NAME/KEY: CDS
49 (B) LOCATION: 262..3078
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
51 CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGGGACA GCGCCGGCCG 60
52 CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGACGTC 120
53 CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA 180
54 GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG 240
55 CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC 291
56 Met Ser Thr Met Arg Leu Leu Thr Leu Ala
57 1 5 10
58 CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC 339
59 Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile
60 15 20 25
61 GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC 387
62 Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe
63 30 35 40
64 CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT 435
65 Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile
66 45 50 55
67 CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG 483
68 Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met
69 60 65 70
70 GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC 531
71 Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile
72 75 80 85 90
73 CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT 579
74 Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro
75 95 100 105
76 GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC 627
77 Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr
78 110 115 120
79 ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG 675
80 Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu
81 125 130 135
82 CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG 723
83 Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met
84 140 145 150
85 ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC 771
86 Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp
87 155 160 165 170
88 CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG 819
89 His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu
90 175 180 185
91 CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG 867

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92 Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys
93 190 195 200
94 AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC 915
95 Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val
96 205 210 215
97 ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA 963
98 Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala
99 220 225 230
100 GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC 1011
101 Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly
102 235 240 245 250
103 GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC 1059
104 Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile
105 255 260 265
106 CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC 1107
107 Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser
108 270 275 280
109 GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG 1155
110 Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys
111 285 290 295
112 GAG AAC ATC ACC GAC CCG CCG CGG TGC GTG GGC AAC ACC AAC ATC 1203
113 Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile
114 300 305 310
115 TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT 1251
116 Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr
117 315 320 325 330
118 GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG 1299
119 Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg
120 335 340 345
121 AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG 1347
122 Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val
123 350 355 360
124 CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG 1395
125 Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys
126 365 370 375
127 ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG 1443
128 Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met
129 380 385 390
130 TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC 1491
131 Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr
132 395 400 405 410
133 GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC 1539
134 Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val
135 415 420 425
136 AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG 1587
137 Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr
138 430 435 440
139 TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT 1635
140 Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe

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141	445	450	455	
142	TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC			1683
143	Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr			
144	460	465	470	
145	GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG			1731
146	Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val			
147	475	480	485	490
148	AAC AAC AGC AAC AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC			1779
149	Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu			
150	495	500	505	
151	AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG			1827
152	Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu			
153	510	515	520	
154	CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG			1875
155	Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu			
156	525	530	535	
157	ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC			1923
158	Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe			
159	540	545	550	
160	ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG			1971
161	Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val			
162	555	560	565	570
163	CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC			2019
164	His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe			
165	575	580	585	
166	GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC			2067
167	Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr			
168	590	595	600	
169	CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC			2115
170	Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly			
171	605	610	615	
172	ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG			2163
173	Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met			
174	620	625	630	
175	GTC TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC			2211
176	Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn			
177	635	640	645	650
178	CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC			2259
179	Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly			
180	655	660	665	
181	ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC			2307
182	Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala			
183	670	675	680	
184	ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG			2355
185	Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu			
186	685	690	695	
187	CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG			2403
188	Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala			
189	700	705	710	

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190 GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC 2451
191 Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile
192 715 720 725 730
193 TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG 2499
194 Trp Asp Ser Ala Val Leu Glu Ala Ser Gln Lys Cys Asp Leu
195 735 740 745
196 GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG 2547
197 Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met
198 750 755 760
199 CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG 2595
200 Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys
201 765 770 775
202 TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG 2643
203 Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg
204 780 785 790
205 TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT 2691
206 Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe
207 795 800 805 810
208 GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC 2739
209 Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala
210 815 820 825
211 GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT 2787
212 Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp
213 830 835 840
214 GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG 2835
215 Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp
216 845 850 855
217 CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT 2883
218 Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro
219 860 865 870
220 AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC 2931
221 Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser
222 875 880 885 890
223 TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC 2979
224 Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Arg
225 895 900 905
226 GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT 3027
227 Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile
228 910 915 920
229 GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC 3075
230 Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser
231 925 930 935
232 TGAGACTCCC CGCCCCCCC CCTCTGCCCT CTCCCCCGCA GACAGACAGA CAGACGGACG 3135
233 GGACAGCGGC CGGGCCACG CAGAGCCCCG GAGCACACG GGGTCGGGG AGGAGCACCC 3195
234 CCAGCCTCCC CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC 3255
235 GTCCCCGGCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTCT 3315
236 ATTTGCAGC AGTACCATCC CACTGATATC ACGGGCCGC TCAACCTCTC AGATCCCTCG 3375
237 GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCCACCTG CCCAGTTAGC CGGGCCAAGG 3435
238 ACACTGATGG GTCCCTGCTGC TCAGGGAAAGGC CTGAGGGAAAG CCCACCCGCC CCAGAGACTG 3495

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\Crf3\RULE60\10007747.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 18
Seq#:47; N Pos. 18
Seq#:49; N Pos. 18
Seq#:51; N Pos. 18
Seq#:53; N Pos. 18
Seq#:57; Xaa Pos.1147,1171
Seq#:58; Xaa Pos.1147,1171

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

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Input Set : N:\Crf3\RULE60\10007747.raw

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L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1493 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1496 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1499 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1502 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1505 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1508 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1511 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1517 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1520 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1523 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1529 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1535 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2813 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2816 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2819 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2822 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2825 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2828 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2831 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2834 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2837 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2840 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2846 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2849 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2852 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2855 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2858 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2861 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2864 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2870 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2873 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2876 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2882 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2885 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3055 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25

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L:3058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3064 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3067 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:9138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:3937
L:9144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:4033
L:9330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1136
L:9334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1168